What is claimed is:

1. A method for detection of Epstein Barr virus nucleic acid in an isolated sample, comprising:

(i) contacting said sample with a probe wherein the probe binds to a target region defined by SEQ. ID NO. 1 or its homologue or a complementary strand thereof, which binding provides a detectable signal, and

(ii) detecting said signal.

2. A method according to Claim 1, further comprising the step of amplifying Epstein Barr virus nucleic acid prior to detecting said signal.

3. A method according to Claim 2, wherein said amplifying step is carried out using a pair of primers, comprising forward and reverse oligonucleotide primers, the forward primer binding to a target site between nucleic acid residues 1-200, preferably 1-100, of the complementary strand of SEQ. ID NO. 1. or its homologue, and the reverse primer binding to a target site between nucleic acid residues 1-500, preferably 100-300, of SEQ. ID NO. 1 or its homologue.

4. A method according to any previous Claim, wherein said probe binds to a target site between nucleic acid residues 1-500, preferably 1-300, of SEQ ID NO. 1 or its homologue or a complementary strand thereof.

5. A method according to any previous Claim wherein said probe is an oligonucleotide probe.

6. A method according to Claim 5 wherein said probe is 1-50 nucleotides long.

7. A method according to Claim 6 wherein said probe is 10-30 nucleotides long.

8. A method according to Claim 6 wherein said probe is 15-25 nucleotides long.

9. A method according to any of Claims 5-8 wherein said probe is of sequence SEQ ID. NO. 2 or 3.

10. A method according to any previous Claim wherein said detectable signal is a change in fluorescence.

11. A method according to Claim 10 wherein the probe is fluorescently labelled.

12. A method according to any of Claims 3 to 11 wherein said forward and reverse oligonucleotide primers are 1 to 50 nucleotides long.

13. A method according to Claim 15 wherein said oligonucleotide primers are 10 to 30 nucleotides long.

14. A method according to Claim 15 wherein said oligonucleotide primers are 15-25 nucleotides long.

15. A method according to any of Claims 12-14 wherein said forward primer is of SEQ. ID NOs. 4 or 5 and said reverse primer is of SEQ. ID Nos. 6 or 7.

16. A method according to any of Claims 3-15 wherein said reverse primer is fluorescently labelled.

17. A method according to any of Claims 3 to 15 wherein said forward primer is fluorescently labelled.

18. A method according to any of Claims 3 to 15 wherein both forward and reverse primers are fluorescently labelled.

19. A probe suitable for use in a method according to any of Claims 1 to 18, wherein said probe binds to a target region defined by SEQ. ID NO. 1 or its homologue or a complementary strand thereof, and said binding provides a detectable signal.

20. A probe according to Claim 19, wherein said probe binds to a target site between nucleic acid residues 1-500, preferably 1-300, of SEQ. ID. NO. 1 or its homologue or a complementary strand thereof.

21. A probe according to Claim 19 or 20 which is an oligonucleotide probe.

22. A probe according to Claim 21 comprising 1-50 nucleotides.

23. A probe according to Claim 21 comprising 10-30 nucleotides.

24. A probe according to Claim 21 comprising 15-25 nucleotides.

25. A probe according to any of Claims 21 to 24 of sequence SEQ. ID NO. 2 or 3.

26. A probe according to any of Claims 19 to 25, wherein said binding is detectable by detecting a change in fluorescence.

27. A probe according to Claim 26, wherein said probe is fluorescently labelled.

28. A pair of oligonucleotide primers, comprising forward and reverse primers, for use in a method according to any of Claims 3 to 18, said forward primer binding to a target site between nucleic acid residues 1-200, preferably 1-100, of the complementary strand of SEQ. ID.

NO. 1 or its homologue, and said reverse primer binding to a target site between nucleic acid residues 1-500, preferably 100-300, of SEQ. ID NO. 1 or its homologue.

29. A pair of primers according to Claim 28, each comprising 1 to 50 nucleotides.

30. A pair of primers according to Claim 29, each comprising 10 to 30 nucleotides.

31. A pair of primers according to Claim 29, each comprising 15 to 25 nucleotides.

32. A pair of primers according to any of Claims 28 to 31, said forward primer of sequence SEQ. ID. NOs. 4 or 5 and said reverse primer of SEQ. ID. NOs. 6 or 7.

33. A pair of primers according to any of Claims 28 to 32 wherein said forward primer and said reverse primer are fluorescently labelled.

34. A forward primer for use in a method according to any of Claims 3 to 18, wherein said forward primer binds to a target site between nucleic acid residues 1-200, preferably 1-100, of the complementary strand of SEQ. ID NO. 1 or its homologue.

35. A forward primer according to Claim 34, comprising 1 to 50 nucleotides.

36. A forward primer according to Claim 35, comprising 10 to 30 nucleotides.

37. A forward primer according to Claim 35, comprising 15 to 25 nucleotides.

38. A forward primer according to any of Claims 34 to 37, of sequence SEQ. ID. NOs. 4 or 5.

39. A forward primer according to any of Claims 34 to 38 wherein said forward primer is fluorescently labelled.

40. A reverse primer for a method according to any of Claims 3-18, wherein said reverse primer binds to a target site between nucleic acid residues 1-500, preferably 100-300, of SEQ. ID NO. 1 or its homologue.

41. A reverse primer according to Claim 40, comprising 1 to 50 nucleotides.

42. A reverse primer according to Claim 41, comprising 10 to 30 nucleotides.

43. A reverse primer according to Claim 41, comprising 15-25 nucleotides.

44. A reverse primer according to any of Claims 40 to 43, of sequence SEQ. ID. NOs. 6 or 7.

45. A reverse primer according to any of Claims 40 to 44 wherein said reverse primer is fluorescently labelled.

46. Use of a probe according to any of Claims 19 to 27 in the manufacture of a composition for detecting Epstein Barr virus nucleic acid.

47. Use of a forward primer according to any of Claims 34 to 39, or a reverse primer according to any of Claims 40 to 45, in the manufacture of a composition for detecting Epstein Barr virus nucleic acid.

48. Use of a pair of primers according to any of Claims 28 to 33 in the manufacture of a composition for detecting Epstein Barr virus nucleic acid.

49. A kit for detection of Epstein Barr virus nucleic acid comprising a probe according to any of Claims 19 to 27 and a pair of primers according to any of Claims 28 to 33.

50. A kit for detection of Epstein Barr virus nucleic acid comprising a probe according to any of Claims 19 to 27 and a forward primer according to any of Claims 34 to 39.

51. A kit for detection of Epstein Barr virus nucleic acid comprising a probe according to any of Claims 19 to 27 and a reverse primer according to any of Claims 40 to 45.

52. A method of quantifying EBV viral load in a first isolated sample, comprising:

(i) contacting said first sample with a probe wherein the probe binds to a target region defined by SEQ. ID NO. 1 or its homologue or a complementary strand thereof, which binding provides a detectable signal, and detecting said signal; and

(ii) comparing the results obtained in step (i) with results obtained using a second, control sample having a known EBV viral load;

and thereby quantifying EBV viral load in the first isolated sample.

53. An in vitro method of monitoring drug efficacy for alleviating EBV infection or an EBV induced medical condition, comprising:

(i) contacting in vitro a first sample with a probe wherein the probe binds to a target region defined by SEQ. ID NO. 1 or its homologue or a complementary strand thereof, which binding provides a detectable signal, and detecting said signal, wherein said first sample has been isolated from a patient; and

(ii) contacting in vitro a second sample with a probe wherein the probe binds to a target region defined by SEQ. ID NO. 1 or its homologue or a complementary strand thereof, which binding provides a detectable signal, and detecting said signal, wherein said second sample has been isolated from a patient after commencement of drug therapy; and

(iii) comparing the results from (i) and (ii) and thereby confirming the efficacy of said drug.

54. A DNA array comprising an immobilised nucleic acid probe that binds to a target region defined by SEQ. ID NO. 1 or its homologue or a complementary strand thereof.

55. A DNA array, wherein the probe is defined according to any of Claims 20-25.

56. A method of detecting Epstein Barr virus nucleic acid in an isolated sample, substantially as hereinbefore described with reference to the description and/ or as shown in the Figures.

57. A forward primer substantially as hereinbefore described with reference to the description and/ or as shown in the Figures.

58. A reverse primer substantially as hereinbefore described with reference to the description and/ or as shown in the Figures.

59. A probe substantially as hereinbefore described with reference to the description and/ or as shown in the Figures.